

#6 1/2



PCT09

RAW SEQUENCE LISTING

DATE: 04/11/2002

PATENT APPLICATION: US/09/868,300

TIME: 16:08:29

Input Set : A:\V300011.app

Output Set: N:\CRF3\04112002\I868300.raw

p.6

ENTERED

3 <110> APPLICANT: De Veylder, Lieven
 4 Boudolf, Veronique
 5 Torres Acosta, Juan A.
 6 Inze, Dirk
 7 <120> TITLE OF INVENTION: NOVEL CELL CYCLE GENES AND USES THEREOF
 8 <130> FILE REFERENCE: 2364/300
 9 <140> CURRENT APPLICATION NUMBER: 09/868,300
 10 <141> CURRENT FILING DATE: 2002-02-26
 11 <150> PRIOR APPLICATION NUMBER: PCT/EP99/10084
 12 <151> PRIOR FILING DATE: 1999-12-17
 13 <150> PRIOR APPLICATION NUMBER: EP 98 12 4062.5
 14 <151> PRIOR FILING DATE: 1998-12-17
 15 <160> NUMBER OF SEQ ID NOS: 58
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 18 <211> LENGTH: 1989
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 20 <213> ORGANISM: Arabidopsis thaliana
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 36 Thr Gln Glu Met Gln Glu Glu Glu Glu Glu Ser Ser Asp Pro Val Phe
 37 1 5 10 15
 38
 39 gat aat gcc atc cag cga gcg ttg att gtt gga gat tac aag gag gcg 97
 40 Asp Asn Ala Ile Gln Arg Ala Leu Ile Val Gly Asp Tyr Lys Glu Ala
 41 20 25 30
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 43 gtg gat cag tgt ata act gca aat aag atg gcc gat gct tta gtt att 145
 44 Val Asp Gln Cys Ile Thr Ala Asn Lys Met Ala Asp Ala Leu Val Ile
 45 35 40 45
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 47 gct cat gtt ggt ggt aca gcg ttg tgg gag agt act cgt gag aaa tat 193
 48 Ala His Val Gly Gly Thr Ala Leu Trp Glu Ser Thr Arg Glu Lys Tyr
 49 50 55 60
 50
 51 ttg aag acg aac agt gcg cca tac atg aag gtt gtt tct gcg atg gtg 241
 52 Leu Lys Thr Asn Ser Ala Pro Tyr Met Lys Val Val Ser Ala Met Val
 53 65 70 75 80
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 55 aac aat gat ctc agg agc ctt atc tat aca agg tca cat aag ttc tgg 289
 56 Asn Asn Asp Leu Arg Ser Leu Ile Tyr Thr Arg Ser His Lys Phe Trp
 57 85 90 95
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 59 aaa gag act ctt gct ctc ctc tgt act ttt gca caa gga gaa caa tgg 337
 60 Lys Glu Thr Leu Ala Leu Leu Cys Thr Phe Ala Gln Gly Glu Gln Trp
 61 100 105 110

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63 aca acc ctg tgt gat gcc ctt gcc tcg aag ttg atg gct gct ggt aac 385
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67 act ttg gct gca gtt ctc tgc tac att tgc gca ggc aat gtt gac aga 433
68 Thr Leu Ala Ala Val Leu Cys Tyr Ile Cys Ala Gly Asn Val Asp Arg
69      130      135      140
71 aca gta gaa att tgg tcg agg agc ctt gca aat gag cgg gat gga aga 481
72 Thr Val Glu Ile Trp Ser Arg Ser Leu Ala Asn Glu Arg Asp Gly Arg
73 145      150      155      160
75 tct tat gct gag ctt ctt caa gat ctt atg gag aag act ctt gtc ctt 529
76 Ser Tyr Ala Glu Leu Leu Gln Asp Leu Met Glu Lys Thr Leu Val Leu
77      165      170      175
79 gct ttg gca act ggc aac aaa aag ttc agc gca tct ctg tgt aaa ctc 577
80 Ala Leu Ala Thr Gly Asn Lys Lys Phe Ser Ala Ser Leu Cys Lys Leu
81      180      185      190
83 ttt gag agt tat gct gag ata ctg gcc agc caa ggg ctt ctt aca acg 625
84 Phe Glu Ser Tyr Ala Glu Ile Leu Ala Ser Gln Gly Leu Leu Thr Thr
85      195      200      205
87 gca atg aag tac ttg aaa gtt ctg gat tct ggt ggc ttg tca cct gaa 673
88 Ala Met Lys Tyr Leu Lys Val Leu Asp Ser Gly Gly Leu Ser Pro Glu
89      210      215      220
91 ctt tca ata tta cgt gat cgt att tct cta tct gca gaa cct gag act 721
92 Leu Ser Ile Leu Arg Asp Arg Ile Ser Leu Ser Ala Glu Pro Glu Thr
93 225      230      235      240
95 aac act aca gct tca gga aac act cag cct caa agc acc atg cca tat 769
96 Asn Thr Thr Ala Ser Gly Asn Thr Gln Pro Gln Ser Thr Met Pro Tyr
97      245      250      255
99 aat cag gag cca act cag gcg caa cca aac gtt ctt gct aac cca tat 817
100 Asn Gln Glu Pro Thr Gln Ala Gln Pro Asn Val Leu Ala Asn Pro Tyr
101      260      265      270
103 gat aat cag tat cag caa ccg tac act gat tct tat tat gtc cct caa 865
104 Asp Asn Gln Tyr Gln Gln Pro Tyr Thr Asp Ser Tyr Tyr Val Pro Gln
105      275      280      285
107 gtt tca cat cca ccc atg cag caa cca acc atg ttt atg cca cac caa 913
108 Val Ser His Pro Pro Met Gln Gln Pro Thr Met Phe Met Pro His Gln
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111 gct cag cca gct ccg cag cca tct ttt act cca gct cct aca agc aat 961
112 Ala Gln Pro Ala Pro Gln Pro Ser Phe Thr Pro Ala Pro Thr Ser Asn
113 305      310      315      320
115 gct cag cca tcc atg aga act aca ttt gtt cct tca act ccc cct gca 1009
116 Ala Gln Pro Ser Met Arg Thr Thr Phe Val Pro Ser Thr Pro Pro Ala
117      325      330      335
119 ctg aag aat gca gat caa tat cag cag cca acc atg agt tct cat tca 1057
120 Leu Lys Asn Ala Asp Gln Tyr Gln Gln Pro Thr Met Ser Ser His Ser
121      340      345      350
123 ttc acg gga cca tct aac aat gca tac cct gtt ccc ccg ggt cct ggt 1105
124 Phe Thr Gly Pro Ser Asn Asn Ala Tyr Pro Val Pro Pro Gly Pro Gly
125      355      360      365
127 caa tat gca cct tct ggc cct tca caa ctt ggg caa tat cct aac cct 1153

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131 aag atg ccc caa gtt gtt gct cca gca gct gga ccc ata gga ttt acg 1201
132 Lys Met Pro Gln Val Val Ala Pro Ala Ala Gly Pro Ile Gly Phe Thr
133 385      390      395      400
135 ccc atg gca act cca gga gtt gct cca aga tct gtg caa cca gca agt 1249
136 Pro Met Ala Thr Pro Gly Val Ala Pro Arg Ser Val Gln Pro Ala Ser
137      405      410      415
139 cct cca aca cag cag gca gct gca cag gca gcc cct gcg cct gca act 1297
140 Pro Pro Thr Gln Gln Ala Ala Ala Gln Ala Ala Pro Ala Pro Ala Thr
141      420      425      430
143 ccg cca cca act gtt cag act gca gat act tcc aac gtt cca gcc cac 1345
144 Pro Pro Pro Thr Val Gln Thr Ala Asp Thr Ser Asn Val Pro Ala His
145      435      440      445
147 cag aaa cct gtg ata gca acg ttg aca agg ctt ttc aat gag aca tcg 1393
148 Gln Lys Pro Val Ile Ala Thr Leu Thr Arg Leu Phe Asn Glu Thr Ser
149      450      455      460
151 gaa gca ctg gga ggc gca cgt gcg aat act act aag aag cgt gag ata 1441
152 Glu Ala Leu Gly Gly Ala Arg Ala Asn Thr Thr Lys Lys Arg Glu Ile
153 465      470      475      480
155 gaa gac aac tcg aga aaa tta ggt gct ctg ttt gtg aaa ctc aac agc 1489
156 Glu Asp Asn Ser Arg Lys Leu Gly Ala Leu Phe Val Lys Leu Asn Ser
157      485      490      495
159 gga gac atc tcc aag aat gct gcg gac aaa ctc gca cag cta tgc caa 1537
160 Gly Asp Ile Ser Lys Asn Ala Ala Asp Lys Leu Ala Gln Leu Cys Gln
161      500      505      510
163 gct ctg gac aac aat gac ttc agc aca gcc ctt caa ata cag gta ctt 1585
164 Ala Leu Asp Asn Asn Asp Phe Ser Thr Ala Leu Gln Ile Gln Val Leu
165      515      520      525
167 ctg act acc agc gaa tgg gac gaa tgc aac ttc tgg ctg gca aca cta 1633
168 Leu Thr Thr Ser Glu Trp Asp Glu Cys Asn Phe Trp Leu Ala Thr Leu
169      530      535      540
171 aag cgg atg atg gtc aag gcc agg caa aat gtg cgg tgattattta 1679
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173 545      550      555
175 ttttctggtt catggatttt tttttttata aattttaagg agggacgtgt gtatcaaact 1739
177 ccttttgctt tcttaatttt ggttttttta aaacgccgtt gctgctctaa tttttttttt 1799
179 tttttttttt tgtcatttat gaacctcatc tgctacttcc agttactttt ttgttttagat 1859
181 agtatagaga tcatcagatt gctgaaacat tttcatgttt ttggatgtta ctttacccga 1919
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193 <400> SEQUENCE: 2
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204		50		55		60										
206	Leu	Lys	Thr	Asn	Ser	Ala	Pro	Tyr	Met	Lys	Val	Val	Ser	Ala	Met	Val
207	65			70		75										80
209	Asn	Asn	Asp	Leu	Arg	Ser	Leu	Ile	Tyr	Thr	Arg	Ser	His	Lys	Phe	Trp
210				85		90										95
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216				115		120										125
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224	Ser	Tyr	Ala	Glu	Leu	Leu	Gln	Asp	Leu	Met	Glu	Lys	Thr	Leu	Val	Leu
225				165		170										175
227	Ala	Leu	Ala	Thr	Gly	Asn	Lys	Lys	Phe	Ser	Ala	Ser	Leu	Cys	Lys	Leu
228				180		185										190
230	Phe	Glu	Ser	Tyr	Ala	Glu	Ile	Leu	Ala	Ser	Gln	Gly	Leu	Leu	Thr	Thr
231				195		200										205
233	Ala	Met	Lys	Tyr	Leu	Lys	Val	Leu	Asp	Ser	Gly	Gly	Leu	Ser	Pro	Glu
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246				275		280										285
248	Val	Ser	His	Pro	Pro	Met	Gln	Gln	Pro	Thr	Met	Phe	Met	Pro	His	Gln
249				290		295										300
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254	Ala	Gln	Pro	Ser	Met	Arg	Thr	Thr	Phe	Val	Pro	Ser	Thr	Pro	Pro	Ala
255				325		330										335
257	Leu	Lys	Asn	Ala	Asp	Gln	Tyr	Gln	Gln	Pro	Thr	Met	Ser	Ser	His	Ser
258				340		345										350
260	Phe	Thr	Gly	Pro	Ser	Asn	Asn	Ala	Tyr	Pro	Val	Pro	Pro	Gly	Pro	Gly
261				355		360										365
263	Gln	Tyr	Ala	Pro	Ser	Gly	Pro	Ser	Gln	Leu	Gly	Gln	Tyr	Pro	Asn	Pro
264				370		375										380
266	Lys	Met	Pro	Gln	Val	Val	Ala	Pro	Ala	Ala	Gly	Pro	Ile	Gly	Phe	Thr
267	385					390						395				400
269	Pro	Met	Ala	Thr	Pro	Gly	Val	Ala	Pro	Arg	Ser	Val	Gln	Pro	Ala	Ser
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279           450           455           460
281 Glu Ala Leu Gly Gly Ala Arg Ala Asn Thr Thr Lys Lys Arg Glu Ile
282 465           470           475           480
284 Glu Asp Asn Ser Arg Lys Leu Gly Ala Leu Phe Val Lys Leu Asn Ser
285           485           490           495
287 Gly Asp Ile Ser Lys Asn Ala Ala Asp Lys Leu Ala Gln Leu Cys Gln
288           500           505           510
290 Ala Leu Asp Asn Asn Asp Phe Ser Thr Ala Leu Gln Ile Gln Val Leu
291           515           520           525
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315 ctc agg tta gga ctt att att gag ggc aaa cga ttg aaa aag cca ccg      95
316 Leu Arg Leu Gly Leu Ile Ile Glu Gly Lys Arg Leu Lys Lys Pro Pro
317           20           25           30
319 act gtt ctc tca cgc ctc tct tct tct ctg gag aga tct ctg tta ctc      143
320 Thr Val Leu Ser Arg Leu Ser Ser Ser Leu Glu Arg Ser Leu Leu Leu
321           35           40           45
323 aat cat gat gac aag att ctg ctt gga tcg cca gac tct gtt acc gtg      191
324 Asn His Asp Asp Lys Ile Leu Leu Gly Ser Pro Asp Ser Val Thr Val
325           50           55           60
327 ttt gac ggg aga tct ccc cct gag atc agt att gca cac tac ttg gat      239
328 Phe Asp Gly Arg Ser Pro Pro Glu Ile Ser Ile Ala His Tyr Leu Asp
329           65           70           75
331 cgc att ttc aag tac tct tgc tgc agt ccc tcc tgc ttc gtc att gcg      287
332 Arg Ile Phe Lys Tyr Ser Cys Cys Ser Pro Ser Cys Phe Val Ile Ala
333 80           85           90           95
335 cat atc tac att gat cac ttt ctc cat aag acc cga gcc ctt ctc aaa      335
336 His Ile Tyr Ile Asp His Phe Leu His Lys Thr Arg Ala Leu Leu Lys
337           100          105          110
339 ccc ctt aat gtc cac cgc ctt atc att aca act gtc atg tta gct gct      383
340 Pro Leu Asn Val His Arg Leu Ile Ile Thr Thr Val Met Leu Ala Ala

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/868,300

DATE: 04/11/2002
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Input Set : A:\V300011.app
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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SECRET